

Figure 1

1284	 TGGCAGAA 	I TTAAAGAA
1274	 	CAAATTAAAAACTTTTAAAAGAA
1264	 CAAAT 	CAAAT
	20 422-432	85283

Figure 2

Evolutionary integration of viral sequences into host genome is a microbial immune subversion strategy

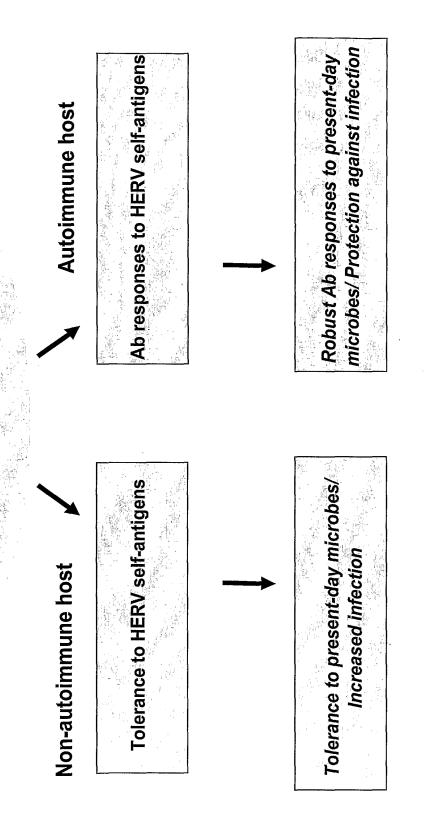


Figure 3

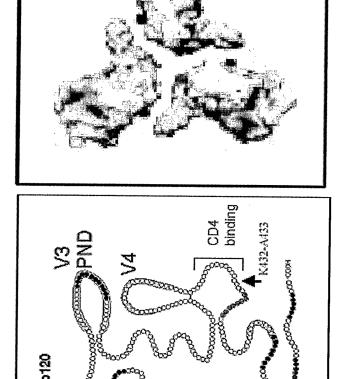


Figure 4

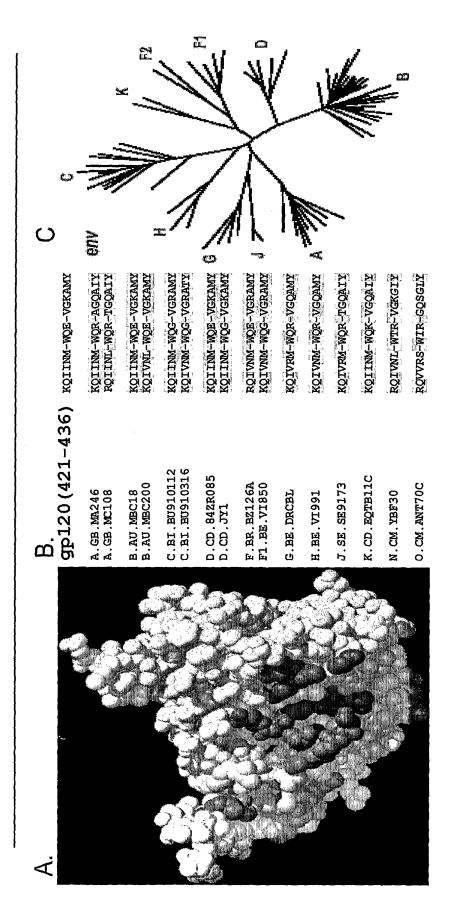
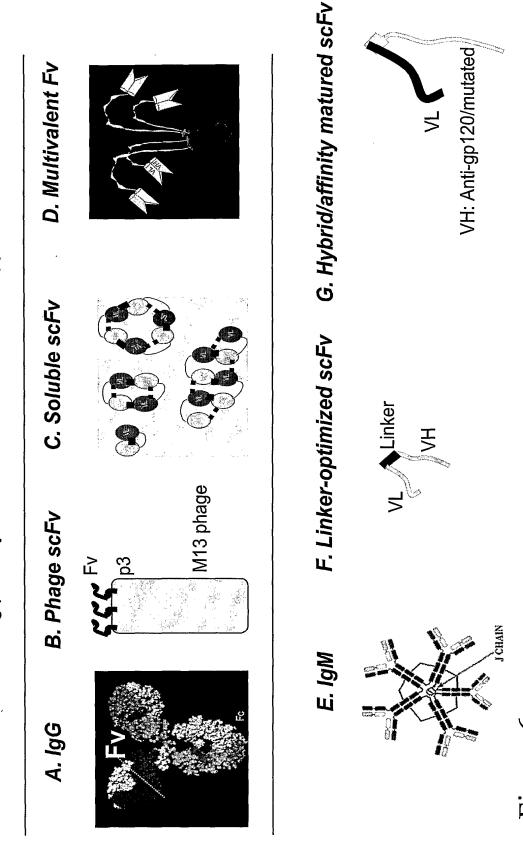


Figure 5

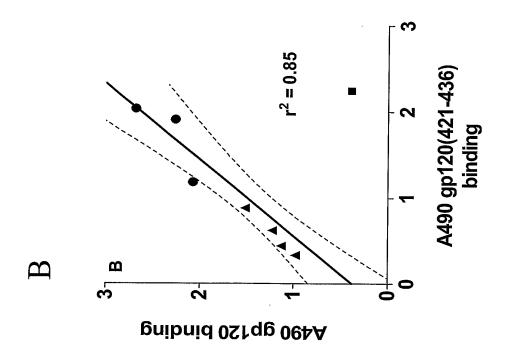
Fv variants with improved gp120 binding properties

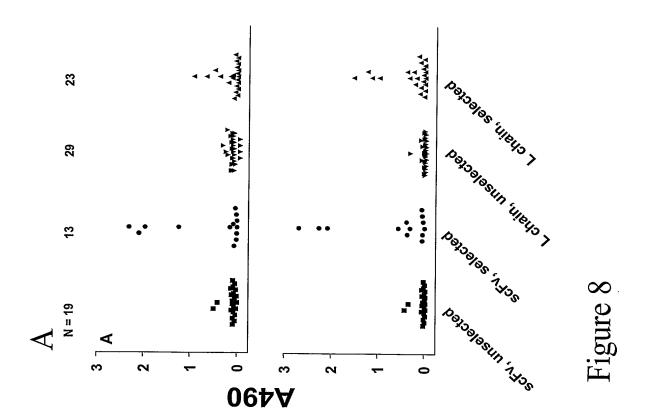
- -- Affinity, avidity, cross-clade HIV neutralization
- -- Neutralizing potency consistent with immunotherapy use



W O 2004/	007730	1 € 1/6/2004/00/002
Antibody expression, mg/L	2 %	[io]
Diversity %	54 100	Inker Hsmyc amper amper amper amper HEN2 amp
Size	8.8×10 ⁵	
Full-length Inserts, %	22 60	Place RBS
Source	PBL, Iupus PBL, Iupus	
Vector	pCT5his6 pHEN2	PHENZ
Library	L chain Fv	99 kD - 72 kD -

Figure '





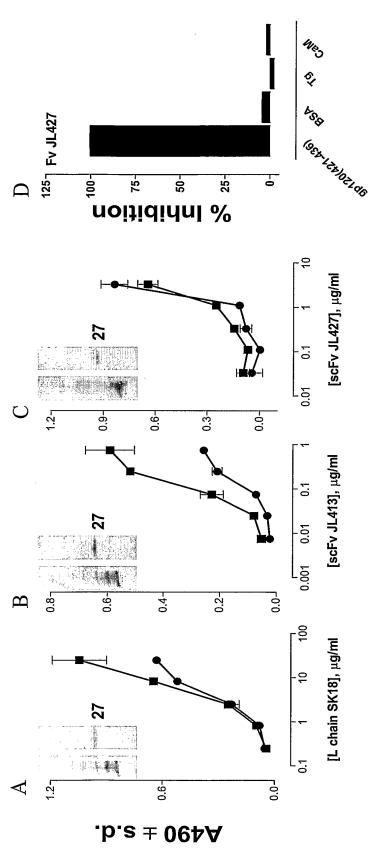


Figure 9

PRO

 ΓXS

SER

PRO

PRO

GLN

THR

GLX

GLY

GLY

PHE

GLN ALA LEU VAL GLY THR

GLU ASP SER ALA THR TYR TYR CYS GIN

101 LYS VAL GLU ILE LYS ARG

THR

VAL

	\triangleright	⊩ -i	д	ש	
	ARG	GLN	VAL	LEU	
	ASP	GEN GEN	ĞĽΥ	SER	
	GLY	TYR	SER	SER	
	VAL	TRP	GEN		
	SER	ALA	LEU	THR	
	ALA	TEU.	SER	LEU THR ILE	
	SER	TRP	SER	THR]	
	VAL	ASN	ALA	PHE	
	SER	ИПВ	GLY	ASP	
	1 ASP VAL VAL MET THR GLN SER PRO SER SER VAL SER ALA SER VAL GLY ASP ARG	ARG ALA SER GEN GLY ILE GLY ASN TRP LEU ALA TRP	TYR GLY ALA SER SER LEU GIN SER GLY VAL	SER GLY SER GLY THR ASP PHE	
	PRO	GLY	ALA HIS ASN LEU LEU ILE	GLY	
	SER	GEN	LEU	SER	
	GLN	SER	LEU	ĞĽΥ	
	THR	ALA	ASN	SER	
	MET	ARG	HIS	ĞГЪ	
in	VAL	CYS	ALA	SER	
dome	VAL	THR	ΓΥS	EHE	
scrv JL413 VL domain	1 ASP	21 ILE	41 GLY	61 ARG	
SCFV					

scFv JL413 VH domain

PRO LEU GLU THR LEU SER LEU GLY PHE THR TYR TYR SER GLY SER THR TYR ASN GLYSER ILE ARG GLN 81 LYS LEU SER SER VAL THR ALA ASP THR ALA MET TYR CYS TRP GLY GLN LYS ASN GLN PHE TRP SER LEU VAL LYS PRO SER TRP SER VAL ASP THR SER TYR SER TYR GLYSER PRO ILE LYS SER ARG VAL THR ILE l GLN VAL ASN LEU ARG GLU SER GLY GLU TRP ILE GLY SER $G\Gamma X$ SER GLY LEU 101 THR LEU VAL THR VAL 21 THR CYS THR VAL 41 PRO GLY LYS

Figure 10 A

scFv JL427 VL domain

60 ILE	PHE	PRO	ARG	VAL	
THR	HIS	VAL	LEU	TRP	
VAL	GLN	GLY	ЗПЭ	GLY	
GEN ARG VAL	TYR	LEU	SER GLY	SER	
GLN	TRP	PRO	ILE	LEU	
GLY	TYR	ARG	ALA	SER	
GLY ALA PRO GLY	CDR1 SER SER SER ASM PHE GLY LEU ASN TYR VAL TYR	TYR ARG ASN ASP GIN ARG PRO LEU	GLY THR SER ALA SER LEU ALA	GIM SER TYR ASP ASN SER LEU SER GLY	
ALA	TYR	ASP	SER	ASP	
GLY	ASN	ASN	ALA	TYR	
SER	THO	ARG	SER	SER	GLY
SER VAL SER	GLY	TYR	THR	GIN	GLY TYR GLN LEU TYR VAL LEU GLY
SER	PHE	ILE	GLY	CYS	VAL
PRO	CDR1	LEU	SER	TYR	TYR
PRO	SER	LEU	GLY SER LYS	TYR	LEU
THR GLN	SER	PRO LYS LEU	SER	ALA ASP	GLN
	SER	PRO	GLY	ALA	TYR
TEU	ĠĽŸ	ALA	SER	GLU	GLY
VAL	SER	THR	PHE	ASP	GLY GLY
SER	CYS	GLY	ARG	GTO	
1 GLN	21 SER	41 PRO	81 ALA	101 SER	121 PHE

scFv JL427 VH domain

60 LEU	ALA	TYR	TYR	E C	
6 ARG L	GLN A	E I	LEU T	ATT TTE	
		A AS		15	~
LEU	ARG	Ħ	THR	ARG	SER
SER	VAL	HIS	ASN	ALA	SER
ARG	TRP	SER	LYS	CYS	VAL
PRO GLY ARG	HIS	GLY	SER	TYR	THR
PRO	MET HIS	SER	ASN	TYR	VAL
GLN	GĽŸ	ARG	ASP	VAL	THR
VAL	TYR	GLY	ARG	ALA	THR
LEU VAL GLN	SER TYR GLY	ILB	SER	THR	GLY
GLY GLY GLY	SER	SER TYR IIB GLY ARG SER GLY SER HIS THR ASN	ILE	ASP	GLN
GLY	PHE	SER	THR	GID	GLY
GLY	THR	VAL 8	PHE	ALA	TRP
SER	PHE	TRP	ARG	ARG	
GEN	ЗТЭ	GLU	GLY	LEU	ASE
GLN	SER	LEU	LYS	SER	MET
LEU	ALA	GLY	VAL	ASN	GLY
VAL GLN	ALA	LYS	SER	ILE	TYR
	CYS	GLY	ASP	GEN	121 PRO ASN TYR GLY MET ASP ILE
1 GLN	41 SER	61 PRO	81 ALA	101 LEU	121 PRO

Figure 10 B

Light chain SK18 VL domain

GHT.	1111		PRO
17 A T.	3		GLN
7 204	2		GTN
7 C D	7		GLN
VAT. CT.V	1		TYR
VAT.	1		TRP
CHD CHD	. Č		ASN
ΔTΩ			LEU ASN
S F F	á		TXR
1.47.1			3 SER SER TYR LEU
C E D	ĺ		SER
C.			TLE
שמ			GLN SER ILE
S F F	á		GLN
CT.N			SER
THR	í.		ARG ALA SER
MFT	1		ARG
N.T.	j		CYS
T	1		THR
η D	Ţ.	21	VAL

80 PRO SER LEU GLN GLY THR ASP PHE THR LEU THR ILE SER 61 ARG PHE SER GLY SER GLY SER

GLY VAL PRO SER

ILE TYR ALA ALA SER SER LEU GLN SER

41 GLY LYS ALA PRO LYS LEU LEU

GLN 81 GLU ASP PHE ALA THR TYR PHE CYS GEN GIN SER TYR SER ILE PRO ARG THR PHE GLY

101 GLY THR LYS VAL GLU ILE LYS

Figure 10 C

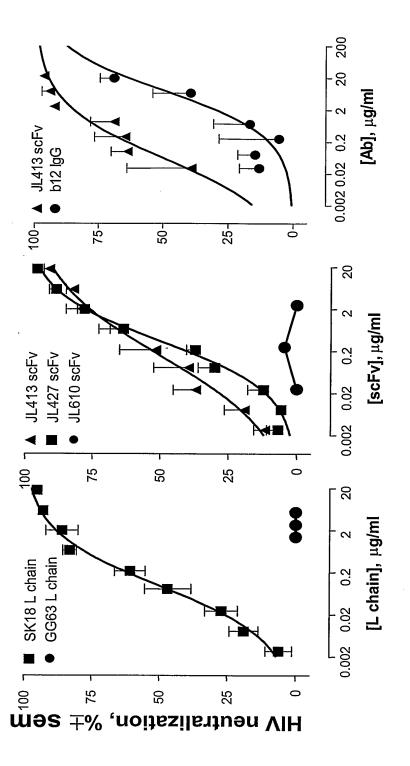


Figure 11